

AB
PATENT & TRADEMARK
Cluster II

cta aaa gta ttt ttt atg agt tca gaa gaa aat aaa gac ttc cgt gct 437
Leu Lys Val Phe Phe Met Ser Ser Glu Glu Asn Lys Asp Phe Arg Ala

125	130	135	
gtg gga ttg aaa acc aaa gca ggc aga gat gag cta tac tgg aaa aca			485
Val Gly Leu Lys Thr Lys Ala Gly Arg Asp Glu Leu Tyr Trp Lys Thr			
140	145	150	155

att aac ctt ttc agtatggt	505
Ile Asn Leu Phe	

<210> 2
 <211> 159
 <212> PRT
 <213> human

<220>
 <221> misc_feature
 <222> (93)..()
 <223> n=a, g, c or t

<400> 2

Met Thr Glu Asn Ser Leu Ser Glu Met Ala Ser Lys Ser Trp Leu Asn
1 5 10 15

Phe Leu Thr Phe Leu Tyr Gly Ser Ala Ile Gly Phe Ile Leu Phe Ser
20 25 30

Gln Leu Leu Ser Ile Leu Leu Gly Glu Glu Gly Asp Thr Gln Thr Asn
35 40 45

Val Leu His Asn Asp Pro His Ala Arg His Ser Asp Asp Asn Gly Gln
50 55 60

Asn His Leu Gly Gly Gln Met Asn Phe Asn Ala Asp Ser Ser Gln Arg
65 70 75 80

Lys Asp Glu Asn Thr Glu Ile Ala Glu Asn Leu Tyr Xaa Gln Val Lys
85 90 95

Ile Leu Cys Trp Val Met Thr Gly Ser Gln Asn Leu Gln Lys Lys Ala
100 105 110

Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys Leu Lys Val Phe Phe
115 120 125

Met Ser Ser Glu Glu Asn Lys Asp Phe Arg Ala Val Gly Leu Lys Thr
130 135 140

Lys Ala Gly Arg Asp Glu Leu Tyr Trp Lys Thr Ile Asn Leu Phe
145 150 155

<210> 3
 <211> 489

<212> DNA
<213> human

<220>
<221> CDS
<222> (55)..(489)

<400> 3

catctaaaaa gactgatgaa gttgattgca aatgctagtc atcataaata ccag aac 57
Asn
1

aca ggt gtc act gac aaa ctc tat caa aag atg aaa att ctt tgc tgg 105
Thr Gly Val Thr Asp Lys Leu Tyr Gln Lys Met Lys Ile Leu Cys Trp
5 10 15

att atg aca gga cct caa aat cta gaa aaa aag atc aga cgc atc aga 153
Ile Met Thr Gly Pro Gln Asn Leu Glu Lys Lys Ile Arg Arg Ile Arg
20 25 30

gat aca tgg gcc cag ggt tgc aat aaa gcg ttg ttt atg agc tca aaa 201
Asp Thr Trp Ala Gln Gly Cys Asn Lys Ala Leu Phe Met Ser Ser Lys
35 40 45

gaa aat aaa gac ttc tct act gtg gga tta cac acc aaa gaa gac aga 249
Glu Asn Lys Asp Phe Ser Thr Val Gly Leu His Thr Lys Glu Asp Arg
50 55 60 65

aac caa ctg tcc tgg aaa ata gtt aaa gct ttt cta tat gct cat gac 297
Asn Gln Leu Ser Trp Lys Ile Val Lys Ala Phe Leu Tyr Ala His Asp
70 75 80

cat tat ctg gaa tac atg gat tgg ttc atg aaa gca gat gat gat ata 345
His Tyr Leu Glu Tyr Met Asp Trp Phe Met Lys Ala Asp Asp Asp Ile
85 90 95

tgt ata tat atc aca ttg gac aac ttg aaa tgg ctt ctc aca aac tat 393
Cys Ile Tyr Ile Thr Leu Asp Asn Leu Lys Trp Leu Leu Thr Asn Tyr
100 105 110

aac cct gat gaa tcc act tac ttt ggg aaa aga ttt aag cac tgc aga 441
Asn Pro Asp Glu Ser Thr Tyr Phe Gly Lys Arg Phe Lys His Cys Arg
115 120 125

aaa cag gac tac atg act gga gga gca gga tat gta ctg agc aaa gaa 489
Lys Gln Asp Tyr Met Thr Gly Gly Ala Gly Tyr Val Leu Ser Lys Glu
130 135 140 145

<210> 4
<211> 145
<212> PRT
<213> human

<400> 4

Asn Thr Gly Val Thr Asp Lys Leu Tyr Gln Lys Met Lys Ile Leu Cys
1 5 10 15

Trp Ile Met Thr Gly Pro Gln Asn Leu Glu Lys Lys Ile Arg Arg Ile
20 25 30

Arg Asp Thr Trp Ala Gln Gly Cys Asn Lys Ala Leu Phe Met Ser Ser
35 40 45

Lys Glu Asn Lys Asp Phe Ser Thr Val Gly Leu His Thr Lys Glu Asp
50 55 60

Arg Asn Gln Leu Ser Trp Lys Ile Val Lys Ala Phe Leu Tyr Ala His
65 70 75 80

Asp His Tyr Leu Glu Tyr Met Asp Trp Phe Met Lys Ala Asp Asp Asp
85 90 95

Ile Cys Ile Tyr Ile Thr Leu Asp Asn Leu Lys Trp Leu Leu Thr Asn
100 105 110

Tyr Asn Pro Asp Glu Ser Thr Tyr Phe Gly Lys Arg Phe Lys His Cys
115 120 125

Arg Lys Gln Asp Tyr Met Thr Gly Gly Ala Gly Tyr Val Leu Ser Lys
130 135 140

Glu
145

<210> 5
<211> 1560
<212> DNA
<213> human

<220>
<221> CDS
<222> (2)..(934)

<400> 5
a gat aat gga cag aat cat cta gaa gga caa atg aac ttc aat gca gat 49
Asp Asn Gly Gln Asn His Leu Glu Gly Gln Met Asn Phe Asn Ala Asp
1 5 10 15

tct agc caa cat aaa gat gag aac aca gac att gct gaa aac ctc tat 97
Ser Ser Gln His Lys Asp Glu Asn Thr Asp Ile Ala Glu Asn Leu Tyr
20 25 30

cag aaa gtt aga att ctt tgc tgg gtt atg acc ggc cct caa aac cta 145
Gln Lys Val Arg Ile Leu Cys Trp Val Met Thr Gly Pro Gln Asn Leu
35 40 45

gag aaa aag gcc aaa cac gtc aaa gct act tgg gcc cag cgt tgt aac 193
Glu Lys Lys Ala Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys Asn
50 55 60

aaa gtg ttg ttt atg agt tca gaa gaa aat aaa gac ttc cct gct gtg 241
Lys Val Leu Phe Met Ser Ser Glu Glu Asn Lys Asp Phe Pro Ala Val
65 70 75 80

gga ctg aaa acc aaa gaa ggc aga gat caa cta tac tgg aaa aca att 289
Gly Leu Lys Thr Lys Glu Gly Arg Asp Gln Leu Tyr Trp Lys Thr Ile
85 90 95

aaa gct ttt cag tat gtt cat gaa cat tat tta caa gat gct gat tgg Lys Ala Phe Gln Tyr Val His Glu His Tyr Leu Gln Asp Ala Asp Trp 100 105 110	337
ttt ttg aaa gca gat gat gac acg tat gtc ata cta gac aat ttg agg Phe Leu Lys Ala Asp Asp Asp Thr Tyr Val Ile Leu Asp Asn Leu Arg 115 120 125	385
tgg ctt ctt tca aaa tac gac cct gaa gaa ccc att tac ttt ggg aga Trp Leu Leu Ser Lys Tyr Asp Pro Glu Glu Pro Ile Tyr Phe Gly Arg 130 135 140	433
aga ttt aag cct tat gta aag cag ggc tac atg agt gga gga gca gga Arg Phe Lys Pro Tyr Val Lys Gln Gly Tyr Met Ser Gly Gly Ala Gly 145 150 155 160	481
tat gta cta agc aaa gaa gcc ttg aaa aga ttt gtt gat gca ttt aaa Tyr Val Leu Ser Lys Glu Ala Leu Lys Arg Phe Val Asp Ala Phe Lys 165 170 175	529
aca gac aag tgt aca cat agt tcc tcc att gaa gac tta gca ctg ggg Thr Asp Lys Cys Thr His Ser Ser Ser Ile Glu Asp Leu Ala Leu Gly 180 185 190	577
aga tgc atg gaa att atg aat gta gaa gca gga gat tcc aga gat acc Arg Cys Met Glu Ile Met Asn Val Glu Ala Gly Asp Ser Arg Asp Thr 195 200 205	625
att gga aaa gaa act ttt cat ccc ttt gtg cca gaa cac cat tta att Ile Gly Lys Glu Thr Phe His Pro Phe Val Pro Glu His His Leu Ile 210 215 220	673
aaa ggt tat cta cct aga acg ttt tgg tac tgg aat tac aac tat tat Lys Gly Tyr Leu Pro Arg Thr Phe Trp Tyr Trp Asn Tyr Asn Tyr Tyr 225 230 235 240	721
cct cct gta gag ggt cct ggt tgc tgc tct gat ctt gca gtt tct ttt Pro Pro Val Glu Gly Pro Gly Cys Cys Ser Asp Leu Ala Val Ser Phe 245 250 255	769
cac tat gtt gat tct aca acc atg tat gag tta gaa tac ctc gtt tat His Tyr Val Asp Ser Thr Thr Met Tyr Glu Leu Glu Tyr Leu Val Tyr 260 265 270	817
cat ctt cgt cca tat ggt tat tta tac aga tat caa cct acc tta cct His Leu Arg Pro Tyr Gly Tyr Leu Tyr Arg Tyr Gln Pro Thr Leu Pro 275 280 285	865
gaa cgt ata cta aag gaa att agt caa gca aac aaa aat gaa gat aca Glu Arg Ile Leu Lys Glu Ile Ser Gln Ala Asn Lys Asn Glu Asp Thr 290 295 300	913
aaa gtg aag tta gga aat cct tgaaagaaaa tcatgaatga acaaaggtaa Lys Val Lys Leu Gly Asn Pro 305 310	964
tatgtctagc actgcactga aaaaggactt ctgcatttct gacatagaac actggaatcc	1024
cagtgaggaa ttctaagtga acatttcctta tagaaacctt tcacatgaat gactataaac	1084
tgaagcttta aatgagctgt gaagtgtgtt aaaatgtgtt ttgatacagt aatatataaa	1144
tatgtctata tatatgagga acttgtgttt tttaaagtgt ggccaggtag aggaactaga	1204

aaagagattt tgttgctgt tttctgacca tctgtgttat tgtcactgag aaactaaaat 1264
 agtaaattta ctaaaactac actgcaccat gtttagtaata aacagatctg ccttaaagaa 1324
 aagaaaattt tagaaagaaa tattgttgct cagtgttggt aatatagctc aagaattgag 1384
 tttatatttg cagtatgcta taaatgatac cccctacca caccacaca cacagttttt 1444
 gtctaataa aatgttgctg tgattattta taattggtag ttttcttcc agaagaagct 1504
 aaaataagac tggcacttac cctgaagtgc attaataaaa ccacacttta aaatta 1560

<210> 6
 <211> 311
 <212> PRT
 <213> human

<400> 6
 Asp Asn Gly Gln Asn His Leu Glu Gly Gln Met Asn Phe Asn Ala Asp
 1 5 10 15

Ser Ser Gln His Lys Asp Glu Asn Thr Asp Ile Ala Glu Asn Leu Tyr
 20 25 30

Gln Lys Val Arg Ile Leu Cys Trp Val Met Thr Gly Pro Gln Asn Leu
 35 40 45

Glu Lys Lys Ala Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys Asn
 50 55 60

Lys Val Leu Phe Met Ser Ser Glu Glu Asn Lys Asp Phe Pro Ala Val
 65 70 75 80

Gly Leu Lys Thr Lys Glu Gly Arg Asp Gln Leu Tyr Trp Lys Thr Ile
 85 90 95

Lys Ala Phe Gln Tyr Val His Glu His Tyr Leu Gln Asp Ala Asp Trp
 100 105 110

Phe Leu Lys Ala Asp Asp Asp Thr Tyr Val Ile Leu Asp Asn Leu Arg
 115 120 125

Trp Leu Leu Ser Lys Tyr Asp Pro Glu Glu Pro Ile Tyr Phe Gly Arg
 130 135 140

Arg Phe Lys Pro Tyr Val Lys Gln Gly Tyr Met Ser Gly Gly Ala Gly
 145 150 155 160

Tyr Val Leu Ser Glu Ala Leu Lys Arg Phe Val Asp Ala Phe Lys
 165 170 175

Thr Asp Thr His Ser Ser Ser Ile Glu Asp Leu Ala Leu Gly
 180 185 190

Arg Cys Met Glu Ile Met Asn Val Glu Ala Gly Asp Ser Arg Asp Thr
195 200 205

Ile Gly Lys Glu Thr Phe His Pro Phe Val Pro Glu His His Leu Ile
210 215 220

Lys Gly Tyr Leu Pro Arg Thr Phe Trp Tyr Trp Asn Tyr Asn Tyr Tyr
225 230 235 240

Pro Pro Val Glu Gly Pro Gly Cys Cys Ser Asp Leu Ala Val Ser Phe
245 250 255

His Tyr Val Asp Ser Thr Thr Met Tyr Glu Leu Glu Tyr Leu Val Tyr
260 265 270

His Leu Arg Pro Tyr Gly Tyr Leu Tyr Arg Tyr Gln Pro Thr Leu Pro
275 280 285

Glu Arg Ile Leu Lys Glu Ile Ser Gln Ala Asn Lys Asn Glu Asp Thr
290 295 300

Lys Val Lys Leu Gly Asn Pro
305 310